



SEQUENCE LISTING

<110> FOLKESSON, Anders; NORMARK, Staffan; LÖFDAHL, Sven

<120> Fimbrial proteins

<130> ABR 022 US

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<141> 2000-05-26

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<160> 11

<170> PatentIn Ver. 2.1

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Leu Gly Gly Arg Met Ser Gly Arg Met Gly Glu Leu Ser Ala Thr Ile	
1065 1070 1075	
agt aac tcc cat caa cgt aat gcg ggc agc gcc agt tca ctc acc gct	5354
Ser Asn Ser His Gln Arg Asn Ala Gly Ser Ala Ser Ser Leu Thr Ala	
1080 1085 1090	
ggc tac agc tcg tct ctg gcg tta tcc cgt aat gga ctg ttc tgg gga	5402
Gly Tyr Ser Ser Leu Ala Leu Ser Arg Asn Gly Leu Phe Trp Gly	
1095 1100 1105 1110	
ggt ggt cag gac ggt gaa ccg gcc tct ggc atg gcg gtg aac gtg gag	5450
Gly Gly Gln Asp Gly Glu Pro Ala Ser Gly Met Ala Val Asn Val Glu	
1115 1120 1125	
tca gag ggg gac gag ggc agt agc ggg aaa gta gtc agc gtt cgt ggc	5498
Ser Glu Gly Asp Glu Gly Ser Ser Gly Lys Val Val Ser Val Arg Gly	
1130 1135 1140	
agc agc cag ccg ttc agt ctc ggt ttt ggt cag cag tcg ctg ttg ctg	5546

Ser Ser Gln Pro Phe Ser Leu Gly Phe Gly Gln Gln Ser Leu Leu Leu  
 1145 1150 1155  
 atg gaa ggc tat aac gcc acg gag gtg acc att gag gat gca ggg gtt 5594  
 Met Glu Gly Tyr Asn Ala Thr Glu Val Thr Ile Glu Asp Ala Gly Val  
 1160 1165 1170  
 agt tca cag ggt atg gca ggc gta aaa gcg gga ggg gga agc agg tgt 5642  
 Ser Ser Gln Gly Met Ala Gly Val Lys Ala Gly Gly Gly Ser Arg Cys  
 1175 1180 1185 1190  
 tac ttc ctg aca ccc ggg cat ctg ctg gtt cac aac atc agc gcc agt 5690  
 Tyr Phe Leu Thr Pro Gly His Leu Leu Val His Asn Ile Ser Ala Ser  
 1195 1200 1205  
 atg agc cga ctg tac gtt ggc cgc gta ctg gac aag gat ggc aga ccg 5738  
 Met Ser Arg Leu Tyr Val Gly Arg Val Leu Asp Lys Asp Gly Arg Pro  
 1210 1215 1220  
 ctg ctg gac gca cag cca ctg aac tat cca ttt ttg tcg ttg gga cct 5786  
 Leu Leu Asp Ala Gln Pro Leu Asn Tyr Pro Phe Leu Ser Leu Gly Pro  
 1225 1230 1235  
 tcc ggg cga ttt agc ctg cag agc gag cat aaa gaa tcc agc ctg tgg 5834  
 Ser Gly Arg Phe Ser Leu Gln Ser Glu His Lys Glu Ser Ser Leu Trp  
 1240 1245 1250  
 ctg ctg tct aaa aac agg atc ctg cgt tgt ccg atg tca gta cat aaa 5882  
 Leu Leu Ser Lys Asn Arg Ile Leu Arg Cys Pro Met Ser Val His Lys  
 1255 1260 1265 1270  
 cgt cgg gat gtt atg cag gta gtg ggt gat gtg cgg tgt gaa tta agt 5930  
 Arg Arg Asp Val Met Gln Val Val Gly Asp Val Arg Cys Glu Leu Ser  
 1275 1280 1285  
 gac gtg gat gcc ctg cca cag gcg ttg caa ata tcg ccg cgg gtc atc 5978  
 Asp Val Asp Ala Leu Pro Gln Ala Leu Gln Ile Ser Pro Arg Val Ile  
 1290 1295 1300  
 cgt ttg ctg aac gtg gca ggt ttg ctg cgc cat tcc gtt cag gaa gcc 6026  
 Arg Leu Leu Asn Val Ala Gly Leu Leu Arg His Ser Val Gln Glu Ala  
 1305 1310 1315  
 tga cgtagagata aaggcggttaa ct atg agt aat aaa atg aag tgg acg agt 6078  
 Met Ser Asn Lys Met Lys Trp Thr Ser  
 1320 1325  
 atg aca gcc cat tgg tca gca att att aat ttc atc cga aaa tat gtt 6126  
 Met Thr Ala His Trp Ser Ala Ile Ile Asn Phe Ile Arg Lys Tyr Val  
 1330 1335 1340  
 tat cca gca agg ata att gcc atc ctg ctg atg gct ggc gct aca ctg 6174  
 Tyr Pro Ala Arg Ile Ile Ala Ile Leu Leu Met Ala Gly Ala Thr Leu  
 1345 1350 1355 1360  
 cca caa gtc gcc gat gcg att acc gtc gac ctg aat tac gac aag aac 6222  
 Pro Gln Val Ala Asp Ala Ile Thr Val Asp Leu Asn Tyr Asp Lys Asn  
 1365 1370 1375  
 aat gta gcg gtc atc act cct gtc tgg tcc caa gaa tgg agt gta gca 6270

Asn Val Ala Val Ile Thr Pro Val Trp Ser Gln Glu Trp Ser Val Ala	
1380 1385 1390	
aat gtg ttg ggg gga tgg gta tgt cgt tca aac agg aat gaa aat gag	6318
Asn Val Leu Gly Gly Trp Val Cys Arg Ser Asn Arg Asn Glu Asn Glu	
1395 1400 1405	
ggg gcg tgt gaa gaa aca cat ttg gta tgg tgg tat gct ttt gga gct	6366
Gly Ala Cys Glu Glu Thr His Leu Val Trp Trp Tyr Ala Phe Gly Ala	
1410 1415 1420	
tat tca aaa att cgt ctg cgt ttc aga gaa caa atc agc cat gcc gaa	6414
Tyr Ser Lys Ile Arg Leu Arg Phe Arg Glu Gln Ile Ser His Ala Glu	
1425 1430 1435 1440	
att acg ctc ata ctg ctc ggc agt gtt cgt gat gcc tgt tat act ggt	6462
Ile Thr Leu Ile Leu Leu Gly Ser Val Arg Asp Ala Cys Tyr Thr Gly	
1445 1450 1455	
gtc atc aac atg aac gct gct gca tgt caa tgg ggt agg tgc ctg aaa	6510
Val Ile Asn Met Asn Ala Ala Ala Cys Gln Trp Gly Arg Ser Leu Lys	
1460 1465 1470	
ctt agg ata cct tca gaa gag ctt gcg aag ata cct aca agc gga aca	6558
Leu Arg Ile Pro Ser Glu Glu Leu Ala Lys Ile Pro Thr Ser Gly Thr	
1475 1480 1485	
tgg aaa gca acg tta gtc ctg gat tat tta caa tgg ggc gga gac gat	6606
Trp Lys Ala Thr Leu Val Leu Asp Tyr Leu Gln Trp Gly Gly Asp Asp	
1490 1495 1500	
cct tta ggc aca tca act aca gat atc acg ctg aat gta aca gac cac	6654
Pro Leu Gly Thr Ser Thr Thr Asp Ile Thr Leu Asn Val Thr Asp His	
1505 1510 1515 1520	
ttt gct gaa aat gcg gct att tac ttt ccg caa ttt ggt aca gca acg	6702
Phe Ala Glu Asn Ala Ala Ile Tyr Phe Pro Gln Phe Gly Thr Ala Thr	
1525 1530 1535	
ccc cgg gtg gac ctg aat ctt cac cgg atg aat gcc tca caa atg tgc	6750
Pro Arg Val Asp Leu Asn Leu His Arg Met Asn Ala Ser Gln Met Ser	
1540 1545 1550	
ggc agg gct aat ctg gat atg tgt ctg tat gac gga ggt gtg aaa gcc	6798
Gly Arg Ala Asn Leu Asp Met Cys Leu Tyr Asp Gly Gly Val Lys Ala	
1555 1560 1565	
cgt tca tta cag atg aag ata gaa gga agc aat aag tca ggt acg gga	6846
Arg Ser Leu Gln Met Lys Ile Glu Gly Ser Asn Lys Ser Gly Thr Gly	
1570 1575 1580	
ttt cag gtt ata aag agc gat tct gct gat acg att gat tat gcg gtc	6894
Phe Gln Val Ile Lys Ser Asp Ser Ala Asp Thr Ile Asp Tyr Ala Val	
1585 1590 1595 1600	
agt atg aat tat ggg gga cga agt att cct gtc acc cgt ggc gtg gag	6942
Ser Met Asn Tyr Gly Gly Arg Ser Ile Pro Val Thr Arg Gly Val Glu	
1605 1610 1615	

ttc agt ctg gat aac gtg gat aaa gca gca acg cgt ccg gtg gta ctt 6990  
 Phe Ser Leu Asp Asn Val Asp Lys Ala Ala Thr Arg Pro Val Val Leu  
 1620 1625 1630

ccc ggg caa cgg cag gcg gta cgt tgt gtg cca gtg ccc ctt acc ctg 7038  
 Pro Gly Gln Arg Gln Ala Val Arg Cys Val Pro Val Pro Leu Thr Leu  
 1635 1640 1645

aca aca caa ccc ttt aac atc aga gag aag cgt tct ggt gag tat cag 7086  
 Thr Thr Gln Pro Phe Asn Ile Arg Glu Lys Arg Ser Gly Glu Tyr Gln  
 1650 1655 1660

gga acg ctg aca gtg aca atg ctg atg gga aca caa acc ccc tga 7131  
 Gly Thr Leu Thr Val Thr Met Leu Met Gly Thr Gln Thr Pro  
 1665 1670 1675

cagtaattat ttattttatt gatattcttc ttatatgggt ttttaaatca gagttctctt 7191

tatatacttg tttttatttaa taaagagaat ctattcactt atgaaaatca atgcgtgagg 7251

ttctgctttc ct atg act gtg tat tta gat gat aaa gat aaa gaa tta ttr 7302  
 Met Thr Val Tyr Leu Asp Asp Lys Asp Lys Glu Leu Leu  
 1680 1685 1690

aaa gaa atc caa aaa gat tgt gca caa act tta tgg caa ctt gca tat 7350  
 Lys Glu Ile Gln Lys Asp Cys Ala Gln Thr Leu Trp Gln Leu Ala Tyr  
 1695 1700 1705

aaa gtg gga ctt acg ccc aca cca tgt ttc aaa cgt tta aaa aaa ctt 7398  
 Lys Val Gly Leu Thr Pro Thr Pro Cys Phe Lys Arg Leu Lys Lys Leu  
 1710 1715 1720

aaa gac agg ggg gtt atc att ggt cag ttc gct tta ttg gat aag gaa 7446  
 Lys Asp Arg Gly Val Ile Ile Gly Gln Phe Ala Leu Leu Asp Lys Glu  
 1725 1730 1735 1740

aaa cta ggt ctt tca ctt aat gtc ttt att atg att aac ata tct gag 7494  
 Lys Leu Gly Leu Ser Leu Asn Val Phe Ile Met Ile Asn Ile Ser Glu  
 1745 1750 1755

gag caa tac gct agt att tct gag aaa ata aag tca atg cct gag gtt 7542  
 Glu Gln Tyr Ala Ser Ile Ser Glu Lys Ile Lys Ser Met Pro Glu Val  
 1760 1765 1770

att gcc ttt tat cga att tct gga tca ttt aat tat tta atg cat aca 7590  
 Ile Ala Phe Tyr Arg Ile Ser Gly Ser Phe Asn Tyr Leu Met His Thr  
 1775 1780 1785

gta ttt aca gat atg aac gat tac tat agt ttt tat gag aaa ata ata 7638  
 Val Phe Thr Asp Met Asn Asp Tyr Tyr Ser Phe Tyr Glu Lys Ile Ile  
 1790 1795 1800

tta act aat tct tca att agt gga tct gca tcg agc ttt gtt ctt gag 7686  
 Leu Thr Asn Ser Ser Ile Ser Gly Ser Ala Ser Ser Phe Val Leu Glu  
 1805 1810 1815 1820

caa ata aag gaa aca aac gaa ctg tca gtg tga aagtgtgatg tgtacttact 7739  
 Gln Ile Lys Glu Thr Asn Glu Leu Ser Val  
 1825 1830

gatttaatac attattatcc ttcttacgga acaacaacgg cagattgagg ctgttgaaca 7799  
aggattttta tccagcagtg tgaaattaag cggcacagaa taacacagcg gaatatcaca 7859  
tggttaaata tccccctg catgtaacaa aaaaccgcat taaaacagat gatgttactg 7919  
atattttttt cgttgaaccc ttctggaaaa aaggcgaaaa ccacataatt gagtcattga 7979  
tgttttttga agagttacaa aagtcattta atttattcaa ccataaatat gggttaaata 8039  
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tatttgcatt gatgatgttc cgttacatta aggaatatac atctgtatct cgttatacgc 8759  
acactcacat tactaatcat tattaatatg agtggtgttc ttgttttacg catgcatggt 8819  
tgcatgtgac gttaaattta aatgagctga ctgtatgaat tctaaatact ttagagaggt 8879  
gttttttgc tcggtagtgt ttatattatt attttatttg gtgttatttg cagccagtgc 8939  
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gatgctactg tagagataat aaattctgct aaagattccc caattcttgt gcattgacat 9059  
cctccacgtc ctgaagggcg tgggttctg ctccaacggg ctgcctgact gcacgctcct 9119  
tccacaggca agcacggcgt gtcccgtctt aaaatgttac gcgcgcggtt tacatcggcg 9179  
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<210> 7

<211> 236

<212> PRT

<213> Salmonella typhi

<400> 7

Met Asn Phe Lys Asp Thr Leu Pro Gly Val Phe Leu Cys Val Ala Met  
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 Phe Ala Cys Gly His Ala Arg Ala Asn Met Leu Val Tyr Pro Met Ala  
 20 25 30  
 Ala Glu Ile Asn Ser Ser Arg Glu Glu Ala Thr Ser Leu Phe Val Tyr  
 35 40 45  
 Ser Lys Ser Asp His Val Gln Tyr Ile Arg Thr Arg Ile Met Arg Ile  
 50 55 60  
 Glu His Pro Gly Met Pro Gln Glu Lys Glu Val Pro Ala Gly Asn Asp  
 65 70 75 80  
 Ile Glu Thr Gly Leu Val Val Ser Pro Glu Lys Phe Ala Leu Ser Pro  
 85 90 95  
 Gly Thr Lys Lys Thr Ile Arg Val Ile Ser Thr Gln Ala Pro Glu Arg  
 100 105 110  
 Glu Glu Ala Trp Arg Val Tyr Phe Glu Ala Val Pro Glu Leu Glu Asp  
 115 120 125  
 Asp Pro Gln Ala Gly Gly Lys Gln Asn Ser Ser Val Ser Val Asn Leu  
 130 135 140  
 Val Trp Gly Val Leu Leu Arg Val Ser Pro Ser Asp Pro Arg Pro Ala  
 145 150 155 160  
 Leu Val Thr Asp Gly His His Leu Leu Asn Thr Gly Asn Thr Arg Leu  
 165 170 175  
 Ser Leu Ile Arg Ala Gly Asn Cys Asp Thr Thr Cys His Trp Gln Asn  
 180 185 190  
 Ile Gly Lys Ser Ile Tyr Pro Gly Gly Ser Ala Asp Ile Pro Ala Gly  
 195 200 205  
 Ile Lys Ser Asn Ala Phe Arg Val Glu Tyr Arg Thr Gly Ala Asn Ser  
 210 215 220  
 Pro Val Ile Ser Ala Asp Leu Thr Ala Ala Gly Lys  
 225 230 235

<210> 8

<211> 191

<212> PRT

<213> Salmonella typhi

<400> 8

Met Tyr Thr Glu Cys Thr Tyr Ile Thr Val Ile Asn Asn Lys Ala Arg  
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 Leu Phe Phe Met Asn Met Lys Thr Ser Phe Ile Ala Ala Ala Val Ala  
 20 25 30  
 Leu Ala Thr Val Tyr Ser Phe Ser Val Ser Ala Val Gln Lys Asp Ile  
 35 40 45

Thr Val Thr Ala Asn Ile Asp Ser Thr Leu Glu Leu Leu Gln Ala Asp  
 50 55 60  
 Gly Ser Ser Leu Pro Ser Thr Met Lys Leu Asp Phe Met Pro Gly Lys  
 65 70 75 80  
 Gly Leu Val His Lys Ser Leu Gln Thr Arg Leu Tyr Ser Asn Asp Gln  
 85 90 95  
 Thr Lys Ser Val Asn Val Lys Leu Leu Asn Ala Pro Gln Leu Ile Asn  
 100 105 110  
 Val Leu Asp Pro Thr Lys Thr Ile Asp Met Glu Val Thr Leu Gly Gly  
 115 120 125  
 Arg Ser Leu Thr Thr Thr Asn Ser Val Leu Glu Ala Lys Thr Leu Phe  
 130 135 140  
 Pro Asp Gly Lys Thr Gly Asp Ala Ser Ala Leu Leu Asn Leu Asp Ile  
 145 150 155 160  
 Gly Gln Lys Ala Gly Ala Ala Leu Gln Asn Leu Pro Ala Gly Glu Tyr  
 165 170 175  
 Ser Gly Leu Val Ser Leu Val Ile Ser Gln Ala Val Thr Ala Gly  
 180 185 190

<210> 9  
 <211> 889  
 <212> PRT  
 <213> Salmonella typhi

<400> 9  
 Met Tyr Tyr Leu Leu Gly Leu Cys Ser Phe Thr Ser Gln Ala Thr Leu  
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 Ile Pro Pro Pro Gly Phe Glu Ser Leu Leu Glu Gly Gln Thr Glu Gln  
 20 25 30  
 Ile Glu Val Leu Leu Pro Gly His Ser Leu Gly Leu Phe Pro Val Val  
 35 40 45  
 Val Lys Pro Asp Thr Val Gln Phe Met Ser Pro Leu Met Val Leu Glu  
 50 55 60  
 Ser Ser Gly Leu Ala Ala Leu Pro Ala Ala Glu Arg Gln Lys Ala Leu  
 65 70 75 80  
 Ala Ala Leu Ser Arg Pro Leu Leu Arg Asn Ser Asn Leu Val Cys Gly  
 85 90 95  
 Val Ser Glu Ala Lys Asp Ser Ser Glu Cys Gly Tyr Val Ala Thr Asp  
 100 105 110  
 Lys Glu Asp Val Ala Val Ile Phe Asp Glu Asn Asn Ala Gln Leu Ser  
 115 120 125



Leu Phe Leu Asn Arg Asp Trp Leu Pro Asp Glu Glu Arg Arg Asp Lys  
 130 135 140  
 Arg Trp Leu Thr Pro Thr Pro Glu Gly Val Ser Ala Phe Ile His Arg  
 145 150 155 160  
 Gln Thr Leu Tyr Leu Ser Asp Asp Leu His Ser Arg Asn Met Thr Leu  
 165 170 175  
 Asn Gly Ser Gly Ala Leu Gly Leu Gly Asp Gly Arg Tyr Leu Gly Gly  
 180 185 190  
 Asp Trp Ala Ala Ile Trp Asn Gln Ser Glu His Tyr Asn Asn Ser Gln  
 195 200 205  
 Ala Trp Phe Asp Asn Leu Phe Val Arg Gln Asp Leu Gly Asn Gln Tyr  
 210 215 220  
 Tyr Leu Gln Ala Gly Arg Met Asp Gln Arg Asn Leu Ser Ser Ala Thr  
 225 230 235 240  
 Gly Gly Asp Phe Gly Phe Ser Leu Leu Pro Leu Ser Arg Phe Asp Gly  
 245 250 255  
 Leu Arg Thr Gly Thr Thr Gln Ala Tyr Val Asn His Glu Val Asp His  
 260 265 270  
 Asn Ala Thr Pro Val Met Val Gln Val Thr Arg Asn Ala Arg Ile Asp  
 275 280 285  
 Ile Tyr Arg Gly Ser Glu Leu Leu Gly Ser Gln Phe Leu Thr Pro Gly  
 290 295 300  
 Met His Thr Leu Asp Thr His Ser Leu Pro Pro Gly Ser Tyr Pro Leu  
 305 310 315 320  
 Ala Leu Arg Val Tyr Glu Asp Gly Ile Leu Arg Arg Thr Glu Thr Gln  
 325 330 335  
 Pro Phe Ser Lys Gly Gly Asn Ser Phe Ser Ala Gln Thr Gln Trp Phe  
 340 345 350  
 Ile Gln Gly Gly Leu Glu Asp Thr Gly Asp Lys Ala Ser His Tyr Asp  
 355 360 365  
 Gly Glu Thr Val Met Ala Ala Gly Phe Gln Thr Gly Leu Arg Lys Asn  
 370 375 380  
 Ile Ser Leu Thr Glu Gly Ile Ser Leu Ala His Glu Ala Trp Tyr Ser  
 385 390 395 400  
 Glu Thr Arg Leu Asn Ser Gln His Ala Val Leu Asp Gly Thr Leu Asp  
 405 410 415  
 Leu Ser Ala Gly Ile Leu His Gly Thr Asp Ser Thr Ser Gly Asn Thr  
 420 425 430  
 Glu Gln Val Thr Tyr Asn Asp Gly Phe Ser Ala Ser Leu Trp Arg Asn  
 435 440 445

His Thr Glu Ser Asp Ala Cys Ser Gly Arg His Pro Gln Ser Val His  
 450 455 460  
 Ala Ser Met Thr Cys Gln Thr Ser Met Asn Ala Ser Leu Ser Val Ser  
 465 470 475 480  
 Val Gly Asn Trp Tyr Ala Leu Leu Gly Tyr Ser Thr Ser Arg Thr Glu  
 485 490 495  
 Gly Arg Pro Val Tyr Arg Gly Tyr Asp Asp Asn Ser Asp Lys Glu Asn  
 500 505 510  
 Val Phe Trp Arg Gln Ala Tyr Ile Pro Ala Ser His Arg Glu Ser Ala  
 515 520 525  
 Gln Ala Ser Ala Thr Tyr Ser Leu Asn Met Ala Gly Met Asn Ile Asn  
 530 535 540  
 Thr His Gly Gly Val Trp Arg Thr Arg Asn Asp Gly Val Asn Asp Asp  
 545 550 555 560  
 Gly Leu Phe Met Ser Val Ser Val Ser Tyr Ala Ser Gln Pro Pro Thr  
 565 570 575  
 Met Thr Gly Ser Asn Arg Tyr Thr Ser Ala Gly Thr Asp Ile His Ser  
 580 585 590  
 Ser Arg Asn Gln Lys Thr Gln Thr Ser Trp Asn Val Asn His Val Arg  
 595 600 605  
 Ser Trp Gln Gln Asp Leu Tyr Arg Glu Leu Ser Val Gly Phe Ser Gly  
 610 615 620  
 Tyr Asn Asp Asp Ser Trp Ser Gly Ser Leu Gly Gly Arg Met Ser Gly  
 625 630 635 640  
 Arg Met Gly Glu Leu Ser Ala Thr Ile Ser Asn Ser His Gln Arg Asn  
 645 650 655  
 Ala Gly Ser Ala Ser Ser Leu Thr Ala Gly Tyr Ser Ser Ser Leu Ala  
 660 665 670  
 Leu Ser Arg Asn Gly Leu Phe Trp Gly Gly Gly Gln Asp Gly Glu Pro  
 675 680 685  
 Ala Ser Gly Met Ala Val Asn Val Glu Ser Glu Gly Asp Glu Gly Ser  
 690 695 700  
 Ser Gly Lys Val Val Ser Val Arg Gly Ser Ser Gln Pro Phe Ser Leu  
 705 710 715 720  
 Gly Phe Gly Gln Gln Ser Leu Leu Leu Met Glu Gly Tyr Asn Ala Thr  
 725 730 735  
 Glu Val Thr Ile Glu Asp Ala Gly Val Ser Ser Gln Gly Met Ala Gly  
 740 745 750  
 Val Lys Ala Gly Gly Gly Ser Arg Cys Tyr Phe Leu Thr Pro Gly His  
 755 760 765

Leu Leu Val His Asn Ile Ser Ala Ser Met Ser Arg Leu Tyr Val Gly  
 770 775 780  
 Arg Val Leu Asp Lys Asp Gly Arg Pro Leu Leu Asp Ala Gln Pro Leu  
 785 790 795 800  
 Asn Tyr Pro Phe Leu Ser Leu Gly Pro Ser Gly Arg Phe Ser Leu Gln  
 805 810 815  
 Ser Glu His Lys Glu Ser Ser Leu Trp Leu Leu Ser Lys Asn Arg Ile  
 820 825 830  
 Leu Arg Cys Pro Met Ser Val His Lys Arg Arg Asp Val Met Gln Val  
 835 840 845  
 Val Gly Asp Val Arg Cys Glu Leu Ser Asp Val Asp Ala Leu Pro Gln  
 850 855 860  
 Ala Leu Gln Ile Ser Pro Arg Val Ile Arg Leu Leu Asn Val Ala Gly  
 865 870 875 880  
 Leu Leu Arg His Ser Val Gln Glu Ala  
 885

<210> 10  
 <211> 359  
 <212> PRT  
 <213> Salmonella typhi

<400> 10  
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 1 5 10 15  
 Ile Ile Asn Phe Ile Arg Lys Tyr Val Tyr Pro Ala Arg Ile Ile Ala  
 20 25 30  
 Ile Leu Leu Met Ala Gly Ala Thr Leu Pro Gln Val Ala Asp Ala Ile  
 35 40 45  
 Thr Val Asp Leu Asn Tyr Asp Lys Asn Asn Val Ala Val Ile Thr Pro  
 50 55 60  
 Val Trp Ser Gln Glu Trp Ser Val Ala Asn Val Leu Gly Gly Trp Val  
 65 70 75 80  
 Cys Arg Ser Asn Arg Asn Glu Asn Glu Gly Ala Cys Glu Glu Thr His  
 85 90 95  
 Leu Val Trp Trp Tyr Ala Phe Gly Ala Tyr Ser Lys Ile Arg Leu Arg  
 100 105 110  
 Phe Arg Glu Gln Ile Ser His Ala Glu Ile Thr Leu Ile Leu Leu Gly  
 115 120 125  
 Ser Val Arg Asp Ala Cys Tyr Thr Gly Val Ile Asn Met Asn Ala Ala  
 130 135 140  
 Ala Cys Gln Trp Gly Arg Ser Leu Lys Leu Arg Ile Pro Ser Glu Glu  
 145 150 155 160

Leu Ala Lys Ile Pro Thr Ser Gly Thr Trp Lys Ala Thr Leu Val Leu  
 165 170 175  
 Asp Tyr Leu Gln Trp Gly Gly Asp Asp Pro Leu Gly Thr Ser Thr Thr  
 180 185 190  
 Asp Ile Thr Leu Asn Val Thr Asp His Phe Ala Glu Asn Ala Ala Ile  
 195 200 205  
 Tyr Phe Pro Gln Phe Gly Thr Ala Thr Pro Arg Val Asp Leu Asn Leu  
 210 215 220  
 His Arg Met Asn Ala Ser Gln Met Ser Gly Arg Ala Asn Leu Asp Met  
 225 230 235 240  
 Cys Leu Tyr Asp Gly Gly Val Lys Ala Arg Ser Leu Gln Met Lys Ile  
 245 250 255  
 Glu Gly Ser Asn Lys Ser Gly Thr Gly Phe Gln Val Ile Lys Ser Asp  
 260 265 270  
 Ser Ala Asp Thr Ile Asp Tyr Ala Val Ser Met Asn Tyr Gly Gly Arg  
 275 280 285  
 Ser Ile Pro Val Thr Arg Gly Val Glu Phe Ser Leu Asp Asn Val Asp  
 290 295 300  
 Lys Ala Ala Thr Arg Pro Val Val Leu Pro Gly Gln Arg Gln Ala Val  
 305 310 315 320  
 Arg Cys Val Pro Val Pro Leu Thr Leu Thr Thr Gln Pro Phe Asn Ile  
 325 330 335  
 Arg Glu Lys Arg Ser Gly Glu Tyr Gln Gly Thr Leu Thr Val Thr Met  
 340 345 350  
 Leu Met Gly Thr Gln Thr Pro  
 355

<210> 11  
 <211> 151  
 <212> PRT  
 <213> Salmonella typhi

<400> 11  
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 Gln Lys Asp Cys Ala Gln Thr Leu Trp Gln Leu Ala Tyr Lys Val Gly  
 20 25 30  
 Leu Thr Pro Thr Pro Cys Phe Lys Arg Leu Lys Lys Leu Lys Asp Arg  
 35 40 45  
 Gly Val Ile Ile Gly Gln Phe Ala Leu Leu Asp Lys Glu Lys Leu Gly  
 50 55 60

Leu Ser Leu Asn Val Phe Ile Met Ile Asn Ile Ser Glu Glu Gln Tyr  
65 70 75 80

Ala Ser Ile Ser Glu Lys Ile Lys Ser Met Pro Glu Val Ile Ala Phe  
85 90 95

Tyr Arg Ile Ser Gly Ser Phe Asn Tyr Leu Met His Thr Val Phe Thr  
100 105 110

Asp Met Asn Asp Tyr Tyr Ser Phe Tyr Glu Lys Ile Ile Leu Thr Asn  
115 120 125

Ser Ser Ile Ser Gly Ser Ala Ser Ser Phe Val Leu Glu Gln Ile Lys  
130 135 140

Glu Thr Asn Glu Leu Ser Val  
145 150